APPENDIX A

Appendix A shows a comparison of the amino acid sequences of the bifunctional LKR-SDH proteins from *Arabidospis* and corn, SEQ ID NO:112 and 122, respectively. Amino acids conserved among both sequences are indicated with an asterisk (*) on the top row; dashes are used by the program to maximize alignment of the sequences. The LKR and SDH domains (boxed sequences) were identified by Epelbaum et al. (*Plant Mol. Biol.* 35:735-748 (1997)) and Tang et al. (*Plant Cell* 9:1305-1316 (1997)).

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                                          ***** ** *       ** ****
SEQ ID: 112  MNSNGHEEEKKLGNGVVGILSETVNKWERRTPLTPSHCARLLHGG-KDRTGISRIVVQPS
SEQ ID: 122  ------------------------------------CARLLLGGGKNGPRVNRIIVQPS


             ****** **   ***** *** **** ***** * ***  *******************
SEQ ID:112   AKRIHHDALYEHVGCEISDDLSDCGLILGIKQPELEMILPERAYAFFSHTHKAQKENMPL
SEQ ID:122   TRRIHHDAQYEDAGCEISEDLSECGLIIGIKQPKLQMILSDRAYAFFSHTHKAQKENMPL


             ********* * ******** *** ***** ****** ********************
SEQ_ID_112   LDKILSERVTLCDYELIVGDHGKRLLAFGKYAGRAGLVDFLHGLGQRYLSLGYSTPFLSL
SEQ_ID_122   LDKILEERVSLFDYELIVGDDGKRSLAFGKFAGRAGLIDFLHGLGQRYLSLGYSTPFLSL


                               LKR domain
             * * ** ********** * ****  *** **** ****** **** ***********
SEQ_ID_112   GASYMYSSLAAAKAAVISVGEEIASQGLPLGICPLVFVFTGTGNVSLAQEIFKLLPHTF
SEQ_ID_122   GQSHMYPSLAAAKAAVIVVAEEIATFGLPSGICPIVFVFTGVGNVSQGAQEIFKLLPHTF


             *    **** *      *      ***** * *** ** * * **** *** ********
SEQ_ID_112   VEPSKLPELFVKDKGISQNGISTKRVYQVYGCIITSQDMVEHKDPSKSFDKADYYAHPEH
SEQ_ID_122   VDAEKLPEIF-QARNLSKQSQSTKRVFQLYGCVVTSRDIVSHKDPTRQFDKGDYYAHPEH


             * ***** * ** ** ********** **   *** *  * **** ***********
SEQ_ID_112   YNPVFHEKISPYTSVLVNCMYWEKRFPCLLSTKQLQDLTKKGLPLVGICDITCDIGGSIE
SEQ_ID_122   YTPVFHERIAPYASVIVNCMYWEKRFPPLLNMDQLQQLMETGCPLVGVCDITCDIGGSIE


             * *  * *  ****  ****** *** * ** * ********* ******** ***  *
SEQ_ID_112   FVNRATLIDSPFFRFNPSNNSYYDDMDGDGVLCMAVDILPTEFAKEASQHFGDILSGFVG
SEQ_ID_122   FINKSTSIERPFFRYDPSKNSYHDDMEGAGVVCLAVDILPTEFSKEASQHFGNILSRLVA


             ****      **  ****** * ** *********       *
SEQ_ID_112   SLASMTEISDLPAHLKRACISYRGELTSLYEYIPRMRKSNPEEAQDNIIANGVSSQRTFN
SEQ_ID_122   SLASVKQPAELPSYLRRACIAHAGRLTPLYEYIPRMRNTMIDLAPAKTNPL---PDKKYS


             ****************** ** ******* ** *** * ********** **
SEQ_ID_112   ILVSLSGHLFDKFLINEALDMIEAAGGSFHLAKCELGQSADAESYSELEVGADDKRVLDQ
SEQ_ID_122   TLVSLSGHLFDKFLINEALDIIETAGGSFHLVRCEVGQSTDDMSYSELEVGADDTATLDK


             ****** ***        *        ****** *        *   *********
SEQ_ID_112   IIDSLTRLANPNEDYISPHREANKISLKIGKVQQ-ENEIKEKPEMTKKSGVLILGAGRVC
SEQ_ID_122   IIDSLTSLANEHGGDHDAGQEIE-LALKIGKVNEYETDVTIDKGSPK---ILILGAGRVC


             **** ****    *        * *       ******* *** *** **    *  *
SEQ_ID_112   RPAADFLASVRTISSQQWYKTYFGADSEEKTDVHVIVASLYLKDAKETVEGISDVEAVRL
SEQ_ID_122   RPAAEFLASYPDICT-------YGVDDHDADQIHVIVASLYQKDAEETVDGIENTTATQL
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SDH domain

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           **  *    **     ****  **  ****** **    *   ****** ******* ***   **
SEQ_ID_112 DVSDSESLLKYVSQVDVVLSLLPASCHAVVAKTCIELKKHLVTASYVDDETSMLHEKAKS
SEQ_ID_122 DVADIGSLSDLVSQVEVVISLLPASFHAAIAGVCIELKKHMVTASYVDESMSNLSQAAKD

           ** *** ********  *  ****   **   *** * **********************
SEQ_ID_112 AGITILGEMGLDPGIDHMMAMKMINDAHIKKGKVKSFTSYCGGLPSPAAANNPLAYKFSW
SEQ_ID_122 AGVTILCEMGLDPGIDHLMSMKMIDEAHARKGKIKAFTSYCGGLPSPAAANNPLAYKFSW

           *****  *  *  *** **   *    *****  ***  **  *  *   *******   *** **  **
SEQ_ID_112 NPAGAIRAGQNPAKYKSNGDIIHVDGKNLYDSAARFRVPNLPAFALECFPNRDSLVYGEH
SEQ_ID_122 NPAGALRSGKNPAVYKFLGETIHVDGHNLYESAKRLRLRELPAFALEHLPNRNSLIYGDL

           ***   ** **  * *  ****** **  **** ****       *     *  *      *    **
SEQ_ID_112 YGIESEATTIFRGTLRYEGFSMIMATLSKLGFFDSEANQVLSTGKRITFGALLSNILNK-
SEQ_ID_122 YGISKEASTIYRATXRYEGFSEIMVTLSKTGFFDAANHPLLQDTSRPTYKGFLDELLNNI

                  *   *     *      *   ***      ****  *   *** *** **    *   * *
SEQ_ID_112 ---DADNESEPLAG-EEEISKRIIKLG--HSKETAAKAAKTIVFLGFNEEREVPSLCKSV
SEQ_ID_122 STINTDLDIEASGGYDDDLIARLLKLGCCKNKEIAVKTVKTIKFLGLHEETQIPKGCSSP

           **  *   **      **   **************     *** *******    **   ****
SEQ_ID_112 FDATCYLMEEKLAYSGNEQDMVLLHHEVEVEFLESKRIEKHTATLLEFGDIKNGQTTTAM
SEQ_ID_122 FDVICQRMEQRMAYGHNEQDMVLLHHEVEVEYPDGQPAEKHQATLLEFGKVENGRSTTAM

           *  ***********  *    *   * **  ***    *  *  *** **    **** *   *
SEQ_ID_112 AKTVGIPAAIGALVLIEDKIKTRGVLRPLEAEVYLPALDILQAYGIKLMEKAE
SEQ_ID_122 ALTVGIPAAIGALLLLKNKVQTKGVIRPLQPEIYVPALEILESSGIKLVEKVF
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